

| | | | | | | | | | | |
|--|--|-------|--------|---------------|---|----------|-------------|------|---|------------|
| Run on: | March 1, 2001, 16:16:52 ; Search time 91.75 Seconds (without alignments) 21.119 Million cell updates/sec | | | | | | | | | |
| Copyright (C) 1993 - 2000 Compugen Ltd. | | | | | | | | | | |
| OM protein - protein search, using sw model | | | | | | | | | | |
| Perfect score: 342 | US-09-331-631A-7_COPY_81_140 | | | | | | | | | |
| Sequence: 1 LQRYQOCGRCQEQQQQR.....HENYHNKKNRSEEEEGQQR | 60 | | | | | | | | | |
| Scoring table: BLOSUM62 | | | | | | | | | | |
| Gapop 10.0 , Gapext 0.5 | | | | | | | | | | |
| Searched: 88757 seqs, 32294092 residues | | | | | | | | | | |
| Total number of hits satisfying chosen parameters: 88757 | | | | | | | | | | |
| Minimum DB seq length: 0 | | | | | | | | | | |
| Maximum DB seq length: 200000000 | | | | | | | | | | |
| Post-processing: Minimum Match 0% | | | | | | | | | | |
| Maximum Match 100% | | | | | | | | | | |
| Listing first 45 summaries | | | | | | | | | | |
| Database : SwissProt_39,* | | | | | | | | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | | | | | |
| 3. SUMMARIES | | | | | | | | | | |
| Result No. | Score | Query | Length | DB ID | Description | RESULT 1 | VCLLA_GOSHI | RPT; | 605 AA. | ALIGNMENTS |
| 1 | 133 | 38.9 | 605 | 1 VCLLA_GOSHI | ID: VCLLA_GOSHI STANDARD; | 1 | 1 | RA | SEQUENCE FROM N.A. | |
| 2 | 132 | 38.6 | 588 | 1 VCLLB_GOSHI | ID: P09799; STANDARD; | 2 | 1 | AC | Chian C.A., Borroto K., Kamalay J.A., Dure L. III; | |
| 3 | 93 | 27.2 | 708 | 1 GBF_DICDI | DT: 01-MAR-1989 (Rel. 10. Created) | 3 | 1 | CC | "Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Sequences and genomic organization of the alpha | |
| 4 | 90.5 | 26.5 | 285 | 1 INVO_CANFA | CC: DT: 01-MAR-1989 (Rel. 10. Last sequence update) | 4 | 1 | CC | VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A). | |
| 5 | 90.5 | 26.5 | 395 | 1 SRY_MOUSE | DE: 15-JUL-1999 (Rel. 38. Last annotation update) | 5 | 1 | CC | Gossypium hirsutum (Upland cotton). | |
| 6 | 90 | 26.3 | 905 | 1 SNF5_YEAST | DT: VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A). | 6 | 1 | CC | Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium. | |
| 7 | 87 | 25.4 | 482 | 1 U2R2_HUMAN | DE: Plant Mol. Biol. 9:533-546(1987). | 7 | 1 | CC | [1] | |
| 8 | 87 | 25.4 | 1154 | 1 WCL1_NEUCR | DP: SEQUENCE FROM N.A. | 8 | 1 | CC | SEQUENCE FROM N.A. | |
| 9 | 86 | 25.1 | 251 | 1 LP61_EIMCR | RA: Chian C.A., Borroto K., Kamalay J.A., Dure L. III; | 9 | 1 | CC | RA: Chian C.A., Borroto K., Kamalay J.A., Dure L. III; | |
| 10 | 86 | 25.1 | 2124 | 1 Y192_HUMAN | RT: "Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Sequences and genomic organization of the alpha | 10 | 1 | CC | RT: "Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Sequences and genomic organization of the alpha | |
| 11 | 85 | 24.9 | 1403 | 1 PRO_DRONE | RT: globulin (vicilin) genes of cottonseed.;" | 11 | 1 | CC | RT: globulin (vicilin) genes of cottonseed.;" | |
| 12 | 84.5 | 24.7 | 648 | 1 KAPC_DICDI | RL: PLANT MOLECULAR BIOLOGY 9:533-546(1987). | 12 | 1 | CC | RL: PLANT MOLECULAR BIOLOGY 9:533-546(1987). | |
| 13 | 84 | 24.6 | 527 | 1 RBFL_CANAL | RP: FUNCTION: SEED STORAGE PROTEIN. | 13 | 1 | CC | RP: FUNCTION: SEED STORAGE PROTEIN. | |
| 14 | 83.5 | 24.4 | 544 | 1 INVO_AOTTR | CC: BODIES | 14 | 1 | CC | CC: BODIES | |
| 15 | 83.5 | 24.4 | 919 | 1 ANDR_HUMAN | -1- SIMILARITY: TO OTHER 75 SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.). | 15 | 1 | CC | -1- SIMILARITY: TO OTHER 75 SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.). | |
| 16 | 83 | 24.3 | 1090 | 1 NITA_NEUCR | CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | 16 | 1 | CC | CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | |
| 17 | 82.5 | 24.1 | 467 | 1 INVOMOUSE | CC: DR: EMBL: M19378; AAA33069.1; -. | 17 | 1 | CC | CC: DR: EMBL: M19378; AAA33069.1; -. | |
| 18 | 82 | 24 | 1905 | 1 TAGB_DICDI | CC: DR: PIR: S06598; S06398. | 18 | 1 | CC | CC: DR: PIR: S06598; S06398. | |
| 19 | 81 | 23.7 | 339 | 1 TFD2_HUMAN | CC: DR: HSSP: P50477; ICAX. | 19 | 1 | CC | CC: DR: HSSP: P50477; ICAX. | |
| 20 | 81 | 23.7 | 758 | 1 YM38_YEAST | CC: DR: INTERPRO: IPR001113; -. | 20 | 1 | CC | CC: DR: INTERPRO: IPR001113; -. | |
| 21 | 81 | 23.7 | 816 | 1 HUNB_DRON | CC: DR: PF00546; Seeds7; 1. | 21 | 1 | CC | CC: DR: PF00546; Seeds7; 1. | |
| 22 | 81 | 23.7 | 1130 | 1 REPT_MOUSE | CC: DR: SIGNAL 1; 23 | 22 | 1 | CC | CC: DR: SIGNAL 1; 23 | |
| 23 | 80.5 | 23.5 | 445 | 1 OC3N_MOUSE | CC: FT: CHAIN 24 | 23 | 1 | CC | CC: FT: CHAIN 24 | |
| 24 | 80 | 23.5 | 445 | 1 OC3N_RAT | CC: SQ: SEQUENCE 605 AA; 71049 MW; C9DB9371C976953B CRC64; | 24 | 1 | CC | CC: SQ: SEQUENCE 605 AA; 71049 MW; C9DB9371C976953B CRC64; | |
| 25 | 80 | 23.4 | 479 | 1 U2R1_HUMAN | CC: Query Match 38.9%; Score 133; DB 1; Length 605; Best Local Similarity 43.3%; Pred. No. 5.5e-06; Matches 26; Conservative 14; Mismatches 18; Indels 2; Gaps 2; | 25 | 1 | CC | CC: Query Match 38.9%; Score 133; DB 1; Length 605; Best Local Similarity 43.3%; Pred. No. 5.5e-06; Matches 26; Conservative 14; Mismatches 18; Indels 2; Gaps 2; | |
| 26 | 80 | 23.4 | 540 | 1 PNR_DROME | CC: QY 3 ROYQOCGRCQEQOGQREGQQCQRCWKEQE-RGEHTH-YHHKKKNFSEEEEGQQR 60 | 26 | 1 | CC | CC: QY 3 ROYQOCGRCQEQOGQREGQQCQRCWKEQE-RGEHTH-YHHKKKNFSEEEEGQQR 60 | |
| 27 | 80 | 23.4 | 1023 | 1 CLOC_DROME | CC: Db 120 KQFKCQQRCQWQPERKQOCVKCREQYQEDPWKGGERENKWRREEEESDEGQQQR 179 | 27 | 1 | CC | CC: Db 120 KQFKCQQRCQWQPERKQOCVKCREQYQEDPWKGGERENKWRREEEESDEGQQQR 179 | |
| 28 | 79.5 | 23.2 | 1898 | 1 TRHY_HUMAN | CC: LEG3_PEA | 28 | 1 | CC | CC: LEG3_PEA | |
| 29 | 79.5 | 23.2 | 47 | 1 AGRP_LUCY | CC: P56568 luffa cylindrica | 29 | 1 | CC | CC: P56568 luffa cylindrica | |
| 30 | 79.5 | 23.2 | 585 | 1 INVO_HUMAN | CC: P07476 hom sapien | 30 | 1 | CC | CC: P07476 hom sapien | |
| 31 | 79.5 | 23.2 | 911 | 1 ANDR_PANTR | CC: P07775 pan troglodytes | 31 | 1 | CC | CC: P07775 pan troglodytes | |
| 32 | 79 | 23.1 | 338 | 1 LEG3_PEA | CC: P14594 pisum sativum | 32 | 1 | CC | CC: P14594 pisum sativum | |
| 33 | 79 | 23.1 | 438 | 1 YOCLB_GOSHI | CC: Q09360 caenorhabditis | 33 | 1 | CC | CC: Q09360 caenorhabditis | |

AC P09801;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VICKLIN C72 PRECURSOR (ALPHAGLOBULIN B).
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Malvales; Malvaceae; Gossypium.
 [1]
 SEQUENCE FROM N A.
 Chian C.A., Pyle J.B., Legocki A.B., Dure L. III;
 RT "Developmental biochemistry of cottonseed embryogenesis and
 germination. XVIII. cDNA and amino acid sequences of the members of
 the storage protein families.";
 RL Plant Mol. Biol. 7:475-489(1986).
 CC -!- FUNCTION: SEED STORAGE PROTEIN.
 CC -!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
 BODIES.
 -!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
 CONVICILIN, CONGLYCLININ, ETC.).

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DR EMBL; T00315; -.
 DR DICTYPB; DB0246; GBPA.
 DR KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
 DR REPEAT.
 FT REPEAT 339 368 1.
 FT DOMAIN 481 510 2.
 FT DOMAIN 11 21 POLY-SER.
 FT DOMAIN 115 263 GLN-RICH.
 FT DOMAIN 270 292 POLY-ASN.
 FT DOMAIN 549 557 POLY ASN.
 SQ SEQUENCE 588 AA; 69729 MW; 63E699B29AB8ADEF CRC64;

Query Match 38.6%; Score 132; DB 1; Length 588;
 Best Local Similarity 35.8%; Pred. No. 6; 7e-06; Indels 22; Gaps 3;
 Matches 29; Conservative 11; Mismatches 19; Indels 22; Gaps 3;

QY 2 ORQYQOCQGRCQEQQQCQREQQCQRCWEOYKED-----ERGEHENYHN 46
 Db 121 ORQFQECQQCHQHQORPERKQOCRCREERYQENPWRERREREEEEEEFGEGEQSHN 180

QY 47 ---HKK---NRSEEEEGOOR 60
 Db 181 PFHFRRSFOSRFREHGNFR 201

RESULT 4
 INVO_CANFA ID INVO_CANFA STANDARD; PRT; 285 AA.
 AC P18171;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE INVOLUCRIN.
 GN IVL.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN [1] Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 SEQUENCE FROM N A.
 RX MEDLINE=90348475; PubMed=2385171;
 RA Tseng H., Green H.;
 RT "The involucrin genes of pig and dog: comparison of their segments of repeats with those of prosimians and higher primates.";
 RL Mol. Biol. Evol. 7:293-302(1990).
 CC -!- FUNCTION: INVOLUCRIN IS A KERATINOCTYE PROTEIN THAT FIRST APPEARS IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.
 CC -!- TISSUE SPECIFICITY: PRESENT IN KERATINOCTYES OF EPIDERMIS AND OTHER STRATIFIED SQUAMOUS EPITHELIUM.

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DR EMBL; M3442; AAA30853.1; -.

RESULT 3
 GBF_DICDI ID GBF_DICDI STANDARD; PRT; 708 AA.
 AC P36417;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE G-BOX BINDING FACTOR (GBF).
 GN GBFA.
 OS Dictyostelium discoideum (Slime mold).
 RN [1] Eukaryota; Dictyosteliida; Dictyostelium.
 SEQUENCE FROM N A., AND PARTIAL SEQUENCE.
 RC STRAIN=AX3;
 RX MEDLINE=91170994; PubMed=812561;
 RA Schnitzler G.R., Fischer W.H., Firtel R.A.;
 RT "Cloning and characterization of the G-box binding factor, an essential component of the developmental switch between early and late development in Dictyostelium.";

Query Match 26.5%; Score 90.5; DB 1; Length 285;
 Best local Similarity 31.7%; Pred. No. 0.031; 18; Indels 5; Gaps 2;
 Matches 19; Conservative 18; Mismatches 18; Indexes 5; Gaps 2;
 SEQUENCE 285 AA; 33384 MW; DCE1BD88B9248BEA CRC64;

Qy 6 OOCQGRQEQCQQGQREQQQCQ--RKQWQEYKQERGEREHENYHNHK--KNRSEEECQQR 60
Db 73 QOCEPQEQEQQQKQEQSEQEQLHLQCLEHQEQESQDQKLYPEQCLEQDQEQQESQDQ 132

RESULT 5

SRY_MOUSE STANDARD PRT; 395 AA.

ID SRY_MOUSE PRT; 395 AA.

AC Q05738; DT 01-JUN-1994 (Rel. 29, Created)
 01-FEB-1996 (Rel. 33, Last sequence update)
 01-NOV-1997 (Rel. 35, Last annotation update)

DE SPX-DETERMINING REGION Y PROTEIN (TESTIS-DETERMINING FACTOR).

GN SRY OR TDY OR TDF.

OS Mus musculus (Mouse).

OC Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteorpha; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1] RP SEQUENCE FROM N.A.

RC STRAIN=129; TISSUE=SPLIEN;

RX MEDLINE=92390368; PubMed=1518820;
 RA Gubbay J., Vivian N., Economou A., Jackson D., Goodfellow P.;
 "Inverted repeat structure of the Sry locus in mice.";
 Proc. Natl. Acad. Sci. U.S.A. 89:7953-7957(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=TORINO; TISSUE=LIVER;

RX MEDLINE=94282071; PubMed=8012385;
 RA Coward P., Nagai K., Chen D., Thomas H.D., Nagamine C.M., Lau Y.-F.C.;
 "Polymorphism of a CAG trinucleotide repeat within Sry correlates with B6.Y(Dom sex reversal)." ;
 Natl. Genet. 6:245-250(1994);

RN [3]

RP SEQUENCE OF 1-124 FROM N.A.

RC STRAIN=129;

RX MEDLINE=90326154; PubMed=2374589;
 RA Gubbay J., Collignon J., Koopman P., Capel B., Economou A., Munsterberg A., Vivian N., Goodfellow P., Lovell-Badge R.;
 "A gene mapping to the sex-determining region of the mouse Y chromosome is a member of a novel family of embryonically expressed genes.";
 Nature 346:245-250(1990).

RN [4]

CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR WHICH REGULATES A GENETIC SWITCH IN MALE DEVELOPMENT. IT IS RESPONSIBLE FOR INITIATING MALE SEX DETERMINATION. SRY HMG BOX RECOGNIZES DNA BY PARTIAL INFERNCALATION IN THE MINOR GROOVE.

CC -!- DOMAIN: THE GLN- AND HIS-RICH DOMAIN MAY MEDIATE PROTEIN-PROTEIN INTERACTIONS.

CC -!- POLYMORPHISM: DIFFERENT ALLELES OCCUR IN STRAINS OF MUS MUSCULUS (MOLLOSSINUS OR DOMESTICUS) IN PARTICULAR THE POLY-GLN REGION IN 167-177 IS POLYMORPHIC WITH EITHER 11, 12 OR 13 GLN. THE NATURE OF THIS POLY-GLN TRACT COULD AFFECT THE PROTEIN'S FUNCTION BY DISTURBING ITS SECONDARY STRUCTURE, PERHAPS BY PREVENTING EFFICIENT CONTACT WITH ANOTHER PROTEIN.

CC -!- SIMILARITY: CONTAINS 1 HMG BOX.

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RESULT 6

SNP5_YEAST STANDARD PRT; 905 AA.

ID SNP5_YEAST PRT; 905 AA.

AC PI8480; DT 01-NOV-1990 (Rel. 16, Created)
 01-OCT-1994 (Rel. 30, Last sequence update)

DB 160 00000FYDHQQQQQQQQQQFHDDHHOOQFHDDHHHHHQEQFHDDHQ 219

Qy 58 QDR 60
Db 220 QQQ 222

Query Match 26.5%; Score 90.5; DB 1; Length 395;
Best local Similarity 28.6%; Pred. No. 0.041; 20; Mismatches 20; Indexes 5; Gaps 2;
Matches 18; Conservative 20; Mismatches 20; Indels 5; Gaps 2;
SEQUENCE FROM N.A.

RC STRAIN=MCY;

RX MEDLINE=91042489; PubMed=2233708;

RA Laurent B.C., Treitel M.A., Carlson M.;

RT "The SNP5 protein of *Saccharomyces cerevisiae* is a glutamine- and proline-rich transcriptional activator that affects expression of a broad spectrum of genes.";

RT Mol. Cell. Biol. 10:5616-5625(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C;

RX MEDLINE=9438722; PubMed=8091861;

RA Holmstrom K., Brandt T., Kallesoe T.;

RT "The sequence of a 32,420 bp segment located on the right arm of chromosome II from *Saccharomyces cerevisiae*.";

RL Yeast 10:S47-S62(1994).

CC -!- FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.

CC -!- SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR COMPLEX.

CC -!- SUBCELLULAR LOCATION: NUCLEAR.

PRO_DROME
ID PRO_DROME STANDARD; PRT; 1403 AA.
AC P29617;
DT 01-APR-1993 (Rel. 25; Created)
DT 01-FEB-1995 (Rel. 33; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE PROTEIN PROSPERO.
GN PRO.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
PT Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
EC Phyoidea; Drosophilidae; Drosophila.
RN [1] SEQUENCE FROM N.A.
RP MEDLINE=92069760; PubMed=1720353;
RA Vaessin H., Grell E., Wolff E., Bier E., Jan L.Y., Jan Y.N.;
PT "Prospero" is expressed in neuronal precursors and encodes a nuclear
protein that is involved in the control of axonal outgrowth in
Drosophila".
RN [2] SEQUENCE FROM N.A.
RP MEDLINE=92171948; PubMed=1540176;
RA Matsuzaki F., Koizumi K., Hama C., Yoshioka T., Nabeshima Y.;
PT "Cloning of the Drosophila Prospero gene and its expression in
ganglion mother cells";
RL Biochem. Biophys. Res. Commun. 182:1326-1332(1992).
RN [3] SEQUENCE FROM N.A.
RP MEDLINE=93083413; PubMed=1842358;
RA Chu-Lagraff G., Wright D.M., McNeil L.K., Doe C.Q.;
PT "The prospero gene encodes a divergent homeodomain protein that
controls neuronal identity in Drosophila";
RL Development Suppl. 2:79-85(1991).
RN [4] SIMILARITY TO C_ELEGANS_CEH-25;
RP MEDLINE=94212446; PubMed=7909177;
RA Buerlein T.R.;
PT "A *Ceenorhabditis elegans* prospero homologue defines a novel domain.",
RL Trends Biochem. Sci. 19:70-71(1994).
CC -!- FUNCTION: INVOLVED IN THE CONTROL OF OTHER NEURONAL PRECURSOR
GENES AS WELL AS AXONAL OUTGROWTH AND PAYING-INDING OF NUMEROUS
CENTRAL AND PERIPHERAL NEURONS. IT IS PROBABLY GENERALLY REQUIRED
FOR PROPER NEURONAL DIFFERENTIATION OF MOST OR ALL NEURONS & THEIR
FOR THE SPECIFICATION OF IDENTITY. PROSPERO PROTEIN MAY REGULATE
TRANSCRIPTION BY BINDING TO DNA.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PROS-L (SHOWN HERE) AND PROS-S;
S; ARE PRODUCED BY ALTERNATIVE SPlicing. THEY HAVE DIFFERENT N-
TERMINAL AMINO ACIDS OF THE HOMEODOMAIN.
CC -!- TISSUE SPECIFICITY: NEURONAL PRECURSORS. EXPRESSED IN THE
DEVELOPING CNS, LENS-SECRETING CONE CELLS OF THE EYE, AND MIDGUT.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN NEURONAL PRECURSORS EARLY DURING
FORMATION.
CC -!- SIMILARITY: BELONGS TO THE PROSPERO FAMILY OF HOMEBOX PROTEINS.
CC
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RESULT 12
KAPC_DICDI ID KAPC_DICDI STANDARD; PRT; 648 AA.
AC P34059;
DT 01-FEB-1994 (Rel. 28; Created)
DT 01-FEB-1994 (Rel. 28; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC 2.7.1.37).
GN PKAC OR PK2 OR FK3.
OS Dictyostelium discoideum (Slime mold);
OC Eukaryota; Dictyosteliida; Dictyostelium.
RN [1] SEQUENCE FROM N.A.
RP MEDLINE=91323730; PubMed=1864510;
RA Buerlein E., Anjard C., Scholder J.-C., Raymond C.D.;
PT "Isolation of two genes encoding putative protein kinases regulated
during dictyostelium development.",
RL Gene 102:57-65(1991).
RN [2] CHARACTERIZATION.
RP MEDLINE=93385080; PubMed=83373760;
RA Anjard C., Etchebehere L., Pinaud S., Veron M., Raymond C.D.;
PT "An unusual catalytic subunit for the cAMP-dependent protein kinase
of Dictyostelium discoideum.",
RL Biochemistry 32:9532-9538(1993).
RN [3] CHARACTERIZATION.
RC STRAIN=AX3;
RX MEDLINE=93066311; PubMed=1332055;
RA Mann S.K.O., Yamamoto W.M., Taylor S.S., Pirtei R.A.;

CC MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE
FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.
CC TISSUE-SPECIFICITY: PRESENT IN KERATINOCTYES OF EPIDERMIS AND
CC OTHER STRATIFIED SQUAMOUS EPITHELIUM.

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CC

EMBL; M25313; AAA35375.1; -.
HSSP; P80220; IDIP.
DR INTERPRO; IPR00354; -.
DR PFAM; PF0004; Involutin.
DR PROSINE; PR00795; INVOLUCRIN; 1.
DR KW Keratinocyte; Repeat.
SQ SEQUENCE 544 AA; 63927 MW; 2A02ABA5E1499F9D CRC64;

Query Match 24.4%; Score 83.5; DB 1; Length 544;
Best Local Similarity 34.8%; Pred. No. 0.25; Mismatches 21; Indels 11; Gaps 3;
Matches 23; Conservatism 11; MisMatches 21; Indels 11; Gaps 3;

Oy 4 QYQOCGCRQCQCGQ---REQQQCORKWQK-----EQEGER--HENYHNHKNRS 52
Db 157 EQEQGOKLCLEQEQEGHLELPQQEQGQIKLCLEQEQGQELPPQQEQGOKLHL 216
Oy 53 EEEEGQ 58
Db 217 EQEQGQ 222

RESULT 15

| | | | |
|------------|---|------|---------|
| ANDR_HUMAN | STANDARD; | PRT; | 919 AA. |
| ID | ANDR_HUMAN | | |
| AC | P10275; | | |
| DT | 01-MAR-1989 (Rel. 10, Created) | | |
| DT | 01-APR-1990 (Rel. 14, Last sequence update) | | |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) | | |
| DE | ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR). | | |
| GN | AR OR NR3C4 OR DHTR. | | |
| OS | Homo sapiens (Human). | | |
| OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo. | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=89112208; PubMed=3216866; | | |
| RA | Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E., French F.S., Wilson E.M.; "The human androgen receptor: complementary deoxyribonucleic acid cloning, sequence analysis and gene expression in prostate.", Mol. Endocrinol. 2:1265-1275(1988). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=90083302; PubMed=2594783; | | |
| RA | Wilson E.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J., Wilson E.M., French F.S.; "Sequence of the intron/exon junctions of the coding region of the human androgen receptor gene and identification of a point mutation in a family with complete androgen insensitivity.", Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989). | | |
| RN | [3] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=90258935; PubMed=2342476; | | |
| RA | Govindan M.V.; "Specific region in hormone binding domain is essential for hormone binding and trans-activation by human androgen receptor.", Mol. Endocrinol. 4:417-427(1990). | | |
| RN | [4] | | |

RP SEQUENCE FROM N.A.

RC TISSUE-PROSTATE;

RC MEDLINE=89017168; PubMed=3174628;

RA Chang C., Kokontis J., Liao S.; "Structural analysis of complementary DNA and amino acid sequences of human and rat androgen receptors.", Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).

RL RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE-PROSTATE;

RC MEDLINE=89088909; PubMed=2911578;

RA Tilley W.D., Marcelli M., Wilson J.D., McPhaul M.J.; "Characterization and expression of a cDNA encoding the human androgen receptor.", Proc. Natl. Acad. Sci. U.S.A. 86:327-331(1989).

RL RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE-PROSTATE;

RC MEDLINE=91155943; PubMed=2293020;

RA Marcelli M., Tilley W.D., Wilson C.M., Griffin J.E., Wilson J.D., McPhaul M.J.; "Definition of the human androgen receptor gene structure permits the identification of mutations that cause androgen resistance: premature termination of the receptor protein at amino acid residue 588 causes complete androgen resistance.", Mol. Endocrinol. 4:1105-1116(1990).

RL RN [7]

RP SEQUENCE OF 189-919 FROM N.A.

RX MEDLINE=8817811; PubMed=335326;

RA Chang C., Kokontis J., Liao S.; "Molecular cloning of human and rat complementary DNA encoding androgen receptors.", Science 240:324-326(1988).

RL RN [8]

RP SEQUENCE OF 468-919 FROM N.A.

RX MEDLINE=88240407; PubMed=3377788;

RA Trapman J., Klaassen P., Kuiper G.G.J.M., van der Korput J.A.G.M., Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorthorst M.M., Mulder E., Brinkmann A.O.; "Cloning, structure and expression of a cDNA encoding the human androgen receptor.", Biochem. Biophys. Res. Commun. 153:241-248(1988).

RL RN [9]

RP POLYMORPHISM OF POLY-GLN REGION.

RX MEDLINE=92220629; PubMed=1561105;

RA Sleddens H.F., Oostra B.A., Brinkmann A.O., Trapman J.; "Trinucleotide repeat polymorphism in the androgen receptor gene (AR).", Nucleic Acids Res. 20:1427-1427(1992).

RL RN [10]

RP POLYMORPHISM OF POLY-GLI REGION.

RC TISSUE-BLOOD;

RA Lu J., Danielsen M.; "Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.", Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

RL RN [11]

RP VARIANTS SBMA IN POLY-GLN REGION.

RX MEDLINE=91287825; PubMed=2062380;

RA La Spada A.R., Wilson E.M., Lubahn D.B., Harding A.E., Fischbeck K.H.; "Androgen receptor gene mutations in X-linked spinal and bulbar muscular atrophy.", Nature 352:77-79(1991).

RL RN [12]

RP REVIEW ON VARIANTS.

RX MEDLINE=95023089; PubMed=1937057;

RA Patterson M.N., Hughes L.A., Gottlieb B., Pinsky L.; "The androgen receptor gene mutations database.", Nucleic Acids Res. 22:3560-3562(1994).

RL RN [13]

RP REVIEW ON VARIANTS.

RX MEDLINE=97169385; PubMed=9016528;

RA Gottlieb B., Trifiro M., Lumbruso R., Vasiliou D.M., Pinsky L.; "The androgen receptor gene mutations database.", Nucleic Acids Res. 25:158-162(1997).

RN [14] VARIANT LNCAP ALA-877.
 RX MEDLINE=91083633; PubMed=2260966;
 RA Veldscholte J., Ris-Stalpers C., Kuiper G.G., Jenster G.,
 RA Berrevoets C., Claassen E., van Rooij H.C.J., Trapman J.,
 RA Brinkmann A.O., Mulder E.;
 RT "A mutation in the ligand binding domain of the androgen receptor of
 human LNCAP cells affects steroid binding characteristics and
 response to anti-androgens.";
 RL Biochem. Biophys. Res. Commun. 173:534-540(1990).
 RN [15] VARIANT CAIS MET-866.
 RX MEDLINE=91186983; PubMed=2082179;
 RA Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J.,
 RA Corton J.L.;
 RT "Functional characterization of naturally occurring mutant androgen
 receptors from subjects with complete androgen insensitivity.";
 RT Mol. Endocrinol. 4:1759-1772(1990).
 RL RN [16] VARIANT CYS-774.
 RP MEDLINE=91310758; PubMed=1856263;
 RA Marcellini M., Tilley W.D., Zoppi S., Griffin J.E., Wilson J.D.,
 RA McPhaul M.J.;
 RT "Androgen resistance associated with a mutation of the androgen
 receptor at amino acid 772 (Arg-->Cys) results from a combination of
 decreased messenger ribonucleic acid levels and impairment of
 receptor function.";
 RL J. Clin. Endocrinol. Metab. 73:318-325(1991).
 RN [17] VARIANT CAIS ASN-695 AND HIS-695, AND SEQUENCE OF 629-723 FROM N.A.
 RX MEDLINE=92131007; PubMed=1775137;
 RA Ris-Stalpers C., Trifiro M.A., Kuiper G.G., Jenster G., Romalo G.,
 RA Sai T., Van Rooij H.C., Kaufman M., Rosenthal R.L., Liao S.;
 RT "Substitution of aspartic acid-686 by histidine or asparagine in the
 human androgen receptor leads to a functionally inactive protein with
 altered hormone-binding characteristics.";
 RT Mol. Endocrinol. 5:1562-1569(1991).
 RN [18] VARIANT CAIS AND PAIS.
 RX MEDLINE=93338440; PubMed=1307250;
 RA Batch J.A., Williams D.M., Davies H.R., Brown B.D., Evans B.A.J.,
 RA Hughes I.A., Patterson M.N.,
 RT "Androgen receptor gene mutations identified by SSCP in fourteen
 subjects with androgen insensitivity syndrome.";
 RL Hum. Mol. Genet. 1:497-503(1992).
 RN [19] VARIANT CATS VAL-787.
 RX MEDLINE=92235226; PubMed=1569163;
 RA Nakao R., Haji M., Yanase T., Ogo A., Takayanagi R., Katsube T.,
 RT "A single amino acid substitution (Met-786-->Val) in the steroid-
 binding domain of human androgen receptor leads to complete androgen
 RT insensitivity syndrome.";
 RL J. Clin. Endocrinol. Metab. 74:1152-1157(1992).
 RN [20] VARIANT LNCAP ALA-877.
 RP MEDLINE=9222955; PubMed=1562539;
 RA Veldscholte J., Berrevoets C.A., Ris-Stalpers C., Kuiper G.G.,
 RA Jenster G., Trapman J., Brinkmann A.O., Mulder E.;
 RT "the androgen receptor in LNCAP cells contains a mutation in the
 RT ligand binding domain which affects steroid binding characteristics
 and response to antiandrogens.";
 RL J. Steroid Biochem. Mol. Biol. 41:665-669(1992).
 RN [21] VARIANT MET-730.
 RX MEDLINE=92335289; PubMed=1631125;
 RA Newmark J.R., Hardy D.O., Tomb D.C., Carter B.S., Epstein J.L.,
 RA Isaacs W.B., Brown T.R., Barrack E.R.;
 RT "Androgen receptor gene mutations in human prostate cancer.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6319-6323(1992).
 RN [22] VARIANT CATS VAL-754.
 RX MEDLINE=93372806; PubMed=8103398;

RN Lobaccaro J.-M., Lumbruso S., Ktari R., Dumas R., Sultan C.;
 RT "An exonic point mutation creates a Maelli site in the androgen
 receptor gene of a family with complete androgen insensitivity
 syndrome.";
 RL Hum. Mol. Genet. 2:1041-1043(1993).
 RN [23] VARIANT CAIS ARG-807.
 RP MEDLINE=94108430; PubMed=8281140;
 RA Akeyemo O., Kallio P.J., Palvimo J.J., Kontula K., Jaenne O.A.;
 RT "A single-base substitution in exon 6 of the androgen receptor gene
 causing complete androgen insensitivity: the mutated receptor fails
 to transactivate but binds to DNA in vitro.";
 RL Hum. Mol. Genet. 2:1809-1812(1993).
 RN [24] VARIANT PAIS VAL-743.
 RP MEDLINE=93315568; PubMed=8325932;
 RA Nakao R., Yanase T., Sakai Y., Haji M., Nawata H.;
 RT "A single amino acid substitution (Gly743 --> Val) in the steroid-
 binding domain of the human androgen receptor leads to Reifenstein
 Query Match 24.4%; Score 83.5; DB 1; Length 919;
 Best Local Similarity 32.3%; Pred. No. 0; 4; Matches 21; Conservative 17; Mismatches 16; Indels 11; Gaps 2;
 Matches 21; Conservative 17; Mismatches 16; Indels 11; Gaps 2;
 QY 1 LQRQYQCQRCQEQQQQRCQQQCRRKWCWQYKEBERGEHENYHKKKNSS-----EE 54
 ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| 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